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RAW SEQUENCE LISTING

DATE: 09/13/2004

PATENT APPLICATION: US/10/600,862A

TIME: 09:42:32

Input Set : A:\39383.txt

Output Set: N:\CRF4\09132004\J600862A.raw

3 <110> APPLICANT: Zankel et al.

5 <120> TITLE OF INVENTION: USE OF THE CHAPERONE RECEPTOR-ASSOCIATED PROTEIN (RAP) FOR

THE

6 DELIVERY OF THERAPEUTIC COMPOUNDS TO THE BRAIN AND OTHER TISSUES

8 <130> FILE REFERENCE: 30610/39383

10 <140> CURRENT APPLICATION NUMBER: US 10/600,862A

11 <141> CURRENT FILING DATE: 2003-06-20

13 <160> NUMBER OF SEQ ID NOS: 28

15 <170> SOFTWARE: PatentIn version 3.2

17 <210> SEQ ID NO: 1

18 <211> LENGTH: 323

19 <212> TYPE: PRT

20 <213> ORGANISM: Homo sapiens

22 <400> SEQUENCE: 1

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 25 1 5 10 15
 28 Gly Glu Glu Phe Arg Met Glu Lys Leu Asn Gln Leu Trp Glu Lys Ala
 29 20 25 30
 32 Gln Arg Leu His Leu Pro Pro Val Arg Leu Ala Glu Leu His Ala Asp
 33 35 40 45
 36 Leu Lys Ile Gln Glu Arg Asp Glu Leu Ala Trp Lys Lys Leu Lys Leu
 37 50 55 60
 40 Asp Gly Leu Asp Glu Asp Gly Glu Lys Glu Ala Arg Leu Ile Arg Asn
 41 65 70 75 80
 44 Leu Asn Val Ile Leu Ala Lys Tyr Gly Leu Asp Gly Lys Lys Asp Ala
 45 85 90 95
 48 Arg Gln Val Thr Ser Asn Ser Leu Ser Gly Thr Gln Glu Asp Gly Leu
 49 100 105 110
 52 Asp Asp Pro Arg Leu Glu Lys Leu Trp His Lys Ala Lys Thr Ser Gly
 53 115 120 125
 56 Lys Phe Ser Gly Glu Glu Leu Asp Lys Leu Trp Arg Glu Phe Leu His
 57 130 135 140
 60 His Lys Glu Lys Val His Glu Tyr Asn Val Leu Leu Glu Thr Leu Ser
 61 145 150 155 160
 64 Arg Thr Glu Glu Ile His Glu Asn Val Ile Ser Pro Ser Asp Leu Ser
 65 165 170 175
 68 Asp Ile Lys Gly Ser Val Leu His Ser Arg His Thr Glu Leu Lys Glu
 69 180 185 190
 72 Lys Leu Arg Ser Ile Asn Gln Gly Leu Asp Arg Leu Arg Arg Val Ser
 73 195 200 205
 76 His Gln Gly Tyr Ser Thr Glu Ala Glu Phe Glu Glu Pro Arg Val Ile
 77 210 215 220
 80 Asp Leu Trp Asp Leu Ala Gln Ser Ala Asn Leu Thr Asp Lys Glu Leu
 81 225 230 235 240



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84 Glu Ala Phe Arg Glu Glu Leu Lys His Phe Glu Ala Lys Ile Glu Lys
85          245          250          255
88 His Asn His Tyr Gln Lys Gln Leu Glu Ile Ala His Glu Lys Leu Arg
89          260          265          270
92 His Ala Glu Ser Val Gly Asp Gly Glu Arg Val Ser Arg Ser Arg Glu
93          275          280          285
96 Lys His Ala Leu Leu Glu Gly Arg Thr Lys Glu Leu Gly Tyr Thr Val
97          290          295          300
100 Lys Lys His Leu Gln Asp Leu Ser Gly Arg Ile Ser Arg Ala Arg His
101 305          310          315          320
103 Asn Glu Leu
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107 <211> LENGTH: 209
108 <212> TYPE: PRT
109 <213> ORGANISM: Homo sapiens
111 <400> SEQUENCE: 2
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114 1          5          10          15
117 Ser Gly Glu Glu Leu Asp Lys Leu Trp Arg Glu Phe Leu His His Lys
118          20          25          30
121 Glu Lys Val His Glu Tyr Asn Val Leu Leu Glu Thr Leu Ser Arg Thr
122          35          40          45
125 Glu Glu Ile His Glu Asn Val Ile Ser Pro Ser Asp Leu Ser Asp Ile
126          50          55          60
129 Lys Gly Ser Val Leu His Ser Arg His Thr Glu Leu Lys Glu Lys Leu
130 65          70          75          80
133 Arg Ser Ile Asn Gln Gly Leu Asp Arg Leu Arg Arg Val Ser His Gln
134          85          90          95
137 Gly Tyr Ser Thr Glu Ala Glu Phe Glu Glu Pro Arg Val Ile Asp Leu
138          100          105          110
141 Trp Asp Leu Ala Gln Ser Ala Asn Leu Thr Asp Lys Glu Leu Glu Ala
142          115          120          125
145 Phe Arg Glu Glu Leu Lys His Phe Glu Ala Lys Ile Glu Lys His Asn
146          130          135          140
149 His Tyr Gln Lys Gln Leu Glu Ile Ala His Glu Lys Leu Arg His Ala
150 145          150          155          160
153 Glu Ser Val Gly Asp Gly Glu Arg Val Ser Arg Ser Arg Glu Lys His
154          165          170          175
157 Ala Leu Leu Glu Gly Arg Thr Lys Glu Leu Gly Tyr Thr Val Lys Lys
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162          195          200          205
165 Leu
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170 <211> LENGTH: 33
171 <212> TYPE: DNA
172 <213> ORGANISM: Artificial sequence
174 <220> FEATURE:
175 <223> OTHER INFORMATION: Synthetic primer

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184 <213> ORGANISM: Artificial sequence
186 <220> FEATURE:
187 <223> OTHER INFORMATION: Synthetic primer
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195 <212> TYPE: PRT
196 <213> ORGANISM: Homo sapiens
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201 1 5 10 15
204 Val Arg Leu Thr Ser Cys Ala Arg Val Leu His Tyr Lys Glu Lys Ile
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208 His Glu Tyr Asn Val Leu Leu Asp Thr Leu Ser Arg Ala Glu Glu Gly
209 35 40 45
212 Tyr Glu Asn Leu Leu Ser Pro Ser Asp Met Thr His Ile Lys Ser Asp
213 50 55 60
216 Thr Leu Ala Ser Lys His Ser Glu Leu Lys Asp Arg Leu Arg Ser Ile
217 65 70 75 80
220 Asn Gln Gly Leu Asp Arg Leu Arg Lys Val Ser His Gln Leu Arg Pro
221 85 90 95
224 Ala Thr Glu Phe Glu Glu Pro Arg Val Ile Asp Leu Trp Asp Leu Ala
225 100 105 110
228 Gln Ser Ala Asn Phe Thr Glu Lys Glu Leu Glu Ser Phe Arg Glu Glu
229 115 120 125
232 Leu Lys His Phe Glu Ala Lys Ile Glu Lys His Asn His Tyr Gln Lys
233 130 135 140
236 Gln Leu Glu Ile Ser His Gln Lys Leu Lys His Val Glu Ser Ile Gly
237 145 150 155 160
240 Asp Pro Glu His Ile Ser Arg Asn Lys Glu Lys Tyr Val Leu Leu Glu
241 165 170 175
244 Glu Lys Thr Lys Glu Leu Gly Tyr Lys Val Lys Lys His Leu Gln Asp
245 180 185 190
248 Leu Ser Ser Arg Val Ser Arg Ala Arg His Asn Glu Leu
249 195 200 205
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253 <211> LENGTH: 3702
254 <212> TYPE: DNA
255 <213> ORGANISM: Artificial sequence
257 <220> FEATURE:
258 <223> OTHER INFORMATION: RAP-GAA fusion sequence
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263	ctcggatcct	actcgcggga	gaagaaccag	cccaagccgt	ccccgaaacg	cgagtccgga	120
265	gaggagtcc	gcatggagaa	gttgaaccag	ctgtgggaga	aggcccagcg	actgcatctt	180
267	cctcccggtga	ggctggccga	gctccacgct	gatctgaaga	tacaggagag	ggacgaactc	240
269	gcctggaaga	aactaaagct	tgacggcttg	gacgaagatg	gggagaagga	agcgagactc	300
271	atacgcaacc	tcaatgtcat	cttggccaag	tatgggtctg	acggaaagaa	ggacgctcgg	360
273	caggtgacca	gcaactccct	cagtggcacc	caggaagacg	ggctggatga	ccccaggtcg	420
275	gaaaagctgt	ggcacaaggc	gaagacctct	gggaaattct	ccggcgaaga	actggacaag	480
277	ctctggcggg	agttcctgca	tcacaaagag	aaagttcacg	agtacaacgt	cctgctggag	540
279	accctgagca	ggaccgaaga	aatccacgag	aacgtcatta	gccccctcga	cctgagcgac	600
281	atcaagggca	gcgtcctgca	cagcaggcac	acggagctga	aggagaagct	gcgcagcatc	660
283	aaccagggcc	tggaccgcct	gcgcagggtc	agccaccagg	gctacagcac	tgaggctgag	720
285	ttcgaggagc	ccagggtgat	tgacctgtgg	gacctggcgc	agtcgcgcaa	cctcacggac	780
287	aaggagctgg	aggcgttccg	ggaggagctc	aagcacttcg	aagccaaaat	cgagaagcac	840
289	aaccactacc	agaagcagct	ggagattgcg	cacgagaagc	tgaggcacgc	agagagcgtg	900
291	ggcgacggcg	agcgtgtgag	ccgcagccgc	gagaagcacg	ccctgctgga	ggggcggacc	960
293	aaggagctgg	gctacacggg	gaagaagcat	ctgcaggacc	tgtccggcag	gatctccaga	1020
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297	tgcgacgtcc	cccccaacag	ccgcttcgat	tgcgccccctg	acaaggccat	caccacaggaa	1140
299	cagtgcgagg	cccgcggtcg	ctgctacatc	cctgcaaagc	aggggctgca	gggagccccag	1200
301	atggggcagc	cctgggtgctt	cttcccaccc	agctacccca	gctacaagct	ggagaacctg	1260
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325	ttcatgcgcg	catactgggg	cctgggcttc	cacctgtgcc	gctggggcta	ctcctccacc	1980
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353	gtcggggccg	acgtctgcgg	cttccctggg	aacacctcag	aggagctgtg	tgtgcgctgg	2820
355	accagctgg	gggccttcta	ccccttcag	cggaaaccaca	acagcctgct	cagtctgccc	2880
357	caggagccgt	acagcttcag	cgagccggcc	cagcaggcca	tgaggaaagg	cctcaccctg	2940
359	cgctacgcac	tcctcccca	cctctacaca	ctgttccacc	aggccacagt	cgcgggggag	3000

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361 accgtggccc ggccctctt cctggagttc cccaaggact ctagcacctg gactgtggac 3060
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365 gaagtgactg gctacttccc cttgggcaca tggtagacc tgcagacggt gccaatagag 3180
367 gcccttggca gcctccacc cccacctgca gctccccgtg agccagccat ccacagcgag 3240
369 gggcagtggg tgacgtgcc ggccccctg gacaccatca acgtccacct ccgggctggg 3300
371 tacatcatcc ccctgcaggg ccctggcctc acaaccacag agtcccgcca gcagcccatg 3360
373 gccctggctg tgccctaac caagggtgga gagggccgag gggagctgtt ctgggacgat 3420
375 ggagagagcc tggagtgct ggagcgaggg gcctacacac aggtcatctt cctggccagg 3480
377 aataacacga tcgtgaatga gctggtacgt gtgaccagtg agggagctgg cctgcagctg 3540
379 cagaaggtga ctgtcctggg cgtggccacg gcgccccagc aggtcctctc caacggtgtc 3600
381 cctgtctcca acttcacct cagccccgac accaagggtc tggacatctg tgtctcgtg 3660
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404 Lys Arg Glu Ser Gly Glu Glu Phe Arg Met Glu Lys Leu Asn Gln Leu
405 35 40 45
408 Trp Glu Lys Ala Gln Arg Leu His Leu Pro Pro Val Arg Leu Ala Glu
409 50 55 60
412 Leu His Ala Asp Leu Lys Ile Gln Glu Arg Asp Glu Leu Ala Trp Lys
413 65 70 75 80
416 Lys Leu Lys Leu Asp Gly Leu Asp Glu Asp Gly Glu Lys Glu Ala Arg
417 85 90 95
420 Leu Ile Arg Asn Leu Asn Val Ile Leu Ala Lys Tyr Gly Leu Asp Gly
421 100 105 110
424 Lys Lys Asp Ala Arg Gln Val Thr Ser Asn Ser Leu Ser Gly Thr Gln
425 115 120 125
428 Glu Asp Gly Leu Asp Asp Pro Arg Leu Glu Lys Leu Trp His Lys Ala
429 130 135 140
432 Lys Thr Ser Gly Lys Phe Ser Gly Glu Glu Leu Asp Lys Leu Trp Arg
433 145 150 155 160
436 Glu Phe Leu His His Lys Glu Lys Val His Glu Tyr Asn Val Leu Leu
437 165 170 175
440 Glu Thr Leu Ser Arg Thr Glu Glu Ile His Glu Asn Val Ile Ser Pro
441 180 185 190
444 Ser Asp Leu Ser Asp Ile Lys Gly Ser Val Leu His Ser Arg His Thr
445 195 200 205
448 Glu Leu Lys Glu Lys Leu Arg Ser Ile Asn Gln Gly Leu Asp Arg Leu
449 210 215 220
452 Arg Arg Val Ser His Gln Gly Tyr Ser Thr Glu Ala Glu Phe Glu Glu
453 225 230 235 240

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